

Fig. 1

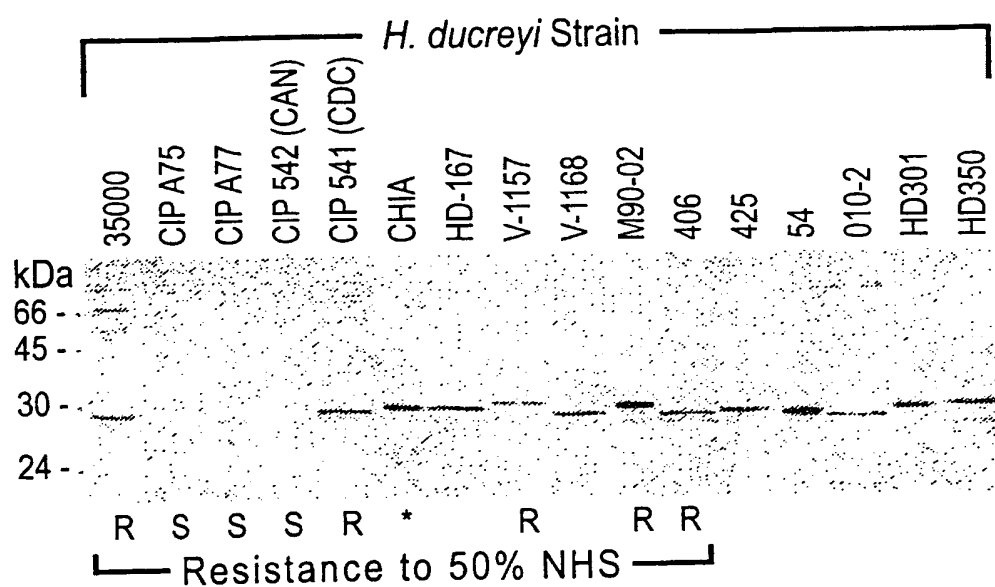


Fig. 2

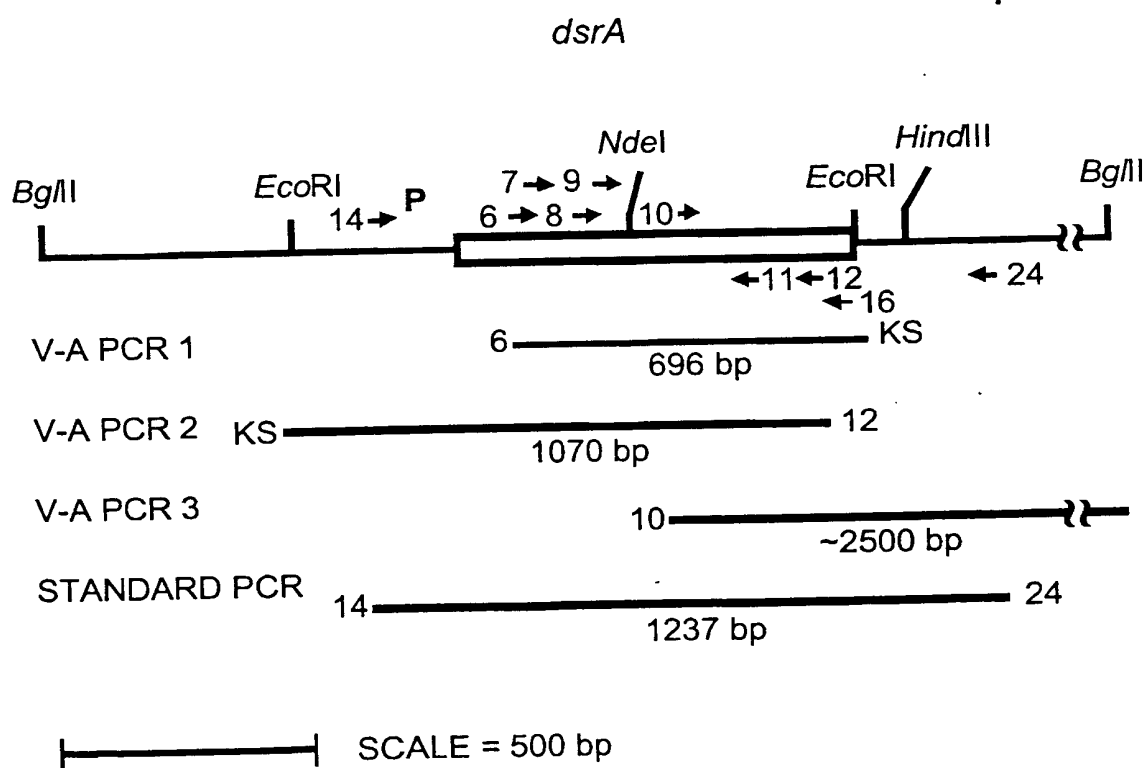


Fig. 3

1 ATAAATACGTCATGACATTTTTTTAATGTAAGGTAGAATAAGAAAGTAAATCTATATTTACAATCAAGATTGACAATTTATTTACTTAATGAGGTGATT
RBS
-35 -10

101 ATGAAAATTAATGTTTAGTTGCCGTAGTGGGATTAGCTTGTCTACTATTACAACAATGGCTCAGCAGCGGCCAAAAGTTTGGCTGGAGTATCTTCTTTGT
1 M K I K C L V A V V G L A C S T I T T M A Q P P K F A G V S S L Y

201 ATAGCTATGAGTATGACTATGGTAAGGGTAAATGGACTTGGTCTAATGAAGGCGGTTTCGATATTAAAGTGCCAGGGGATTAAATGAAGCCAAAAGAATG
35 S Y E Y D Y G K G K W T W S N E G G F D I K V P G I K M K P K E W

301 GATTCTAAACAGGCTACTTATCTTGAATTACAGCATTTATATGCCCTTATCTCTGTTCTCGTGACATATGCTCCTGGCGTTTCTCCTAGCCCTATACTG
68 I S K Q A T Y L E L Q H Y M P Y T P V L V T Y A P G V S P S P I L

401 TTATATCCGATGTCTGATCCTGATCAACTTGGAAATAATCGGCAGCAGCTGAAATTTGAATTTGTATAGTTATTTTAAACGATTAAAGACACGATTTTAAAT
101 L Y P M S D P D Q L G I N R Q Q L K L N L Y S Y F N D L R H D F K L

501 TAAAGTCTTGATGCACGTATTTCCAAAAATAAAACAAAAATATTGATACATAAGTAAATATTACTAGAACTGGGTACTTATTTAGATGATCTTATCG
135 K V L D A R I S K N K Q N I D T I S K Y L L E L G T Y L D D S Y R

601 TATGATGGAACAAAAATACACATAATATCAATAAAGTTGTCTAAAGAAATGCAAACTGGTTTAGCCAAACCAATCAGCATTTCTATGTTAGTGCAACCAAT
168 M M E Q N T H N I N K L S K E L Q T G L A N Q S A L S M L V Q P N

701 GGTGTAGGCAAAACGAGCGTTTCTGCTGCGGTAGGAGGTTATAGAGATAAACTGCATTAGCCATTGGTGTGCGGTACGCAATTTACTGATCGCTTTACCG
201 G V G K T S V S A A V G G Y R D K T A L A I G V G S R I T D R F T A

801 CTAAAGCGGTAGCGTTCAATACCTACATGGCGGCATGTCTTATGGTCTTCTGTTGGTTATGAATTCATTAATCACTAATCGTTT
235 K A G V A F N T Y N G G M S Y G A S V G Y E F *

901 TGGTTATAATAAAAGGCTAAATGTTTCTCCTCACATTTAGCCCTTCTTATTTATAGCTTTTGTCTGTTATAAAACCGTTTCTTTTAGCCACTT
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Fig. 4

DsrA	1	QPPKE	6
UspA2	1	QVVEQFPNFFNENHDELDDAYHNMILGDTAIVSNSQDNSTQLKFYNDESDVPDLSLLFSKLLHEQQNLNGFKAGDTIIPLDKDGKPVYT	90
YadA	1	-----DDYDGIPNLTA VQISPNDPALGLEYPVRPPVPGA-----GGLNASAKGIHSIAIGATAEA-----	56
DsrA	7	-----AGVSSLSY-----EX-----DYG-----KGWT-----WSNE	29
UspA2	46	KDTRTKDGKVEVTVSVTTKIATQDDVEQSAYSRGIQGDIDDLIDINREVNEMLKATHDYNERTQTEAIDALNKASSANTDRIDTA EERIDK	180
YadA	57	-----AKGA AVAGAGSIATGVNS-----VAIGPL-----SKALGD-----SAVTYGAASTAQKDGVAIGARASTSDTGVA-----	117
DsrA	30	GGFDIK	55
UspA2	181	NEYDIKALESNVEEGLLELSGHLIDQKADLTQDKIKALESNVEEGLLDLSGRLLDQKADI AK	270
YadA	118	VGFSKADAKN-----SVAIGHSSHVAANHGYSIAIGDRSKTDRENSVSIGHESLNRLTHLAAGTKD-----TDAVNVAQLKKEIEK	195
DsrA	56	LOHYMPYTPVLVTYAPGVSPSPILIPYPMSPDQGLNROQLKI-----NEYSYFNDL-RHDFKLKVLD-----ARIS	121
UspA2	271	NQADIAQNQTDIODLAAYNELODAYAKQOTE AIDALNKASSENTONTAKNQADITANNINNIYELAQOQDQHSPIKTLAKASAANTDRIA	360
YadA	196	TQENTNKRSAELLANAN-----AYADNKSSSV-----LGIANNYTDKSAETLENARKEAFA-----QSKDVLMMAKAHSNSVAR-----	265
DsrA	122	KNKQNDTJ-----SKY-----LEELGT-----Y-----LDDSI	144
UspA2	361	KNKADADASFETLTKNQNTLIEKDKHEHKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSIIDLGTKVVDGFDGRVTALDTK	450
YadA	266	-----TLETAEEHANSV-----ARTTLETAEE-----HANKKSAEALASANVYADSKSSHTL-KTANSYTDVTS-----NSTKKAIR ES	335
DsrA	145	YRMMEQNTHN-----ENKLSKEIOTGLANOSATSMIAVQPNGVGKTSVSAAVGGYRDKTALALGVGSRITDRTAKAGVAFNINNGGM-SYG	229
UspA2	451	ANALDTKYNAPDGRITIALDSKYENGMAQANISGLFQPYSVGKFNATAALGGYGSKSVAIGAGYRVNPNLAFKAGAAINTSGNKKGSYN	540
YadA	336	NQYTDHKFRQLDNRLDKDTRVDKGLASSAAANSLFQPYGVGKVNFTAGVGGYRSQALALGSGYRVNENVALKAGVAYAGSSDVM--YN	423
DsrA	230	ASVGGEF	
UspA2	541	IGVNIYEF	
YadA	424	ASFNI EW	

Fig. 5

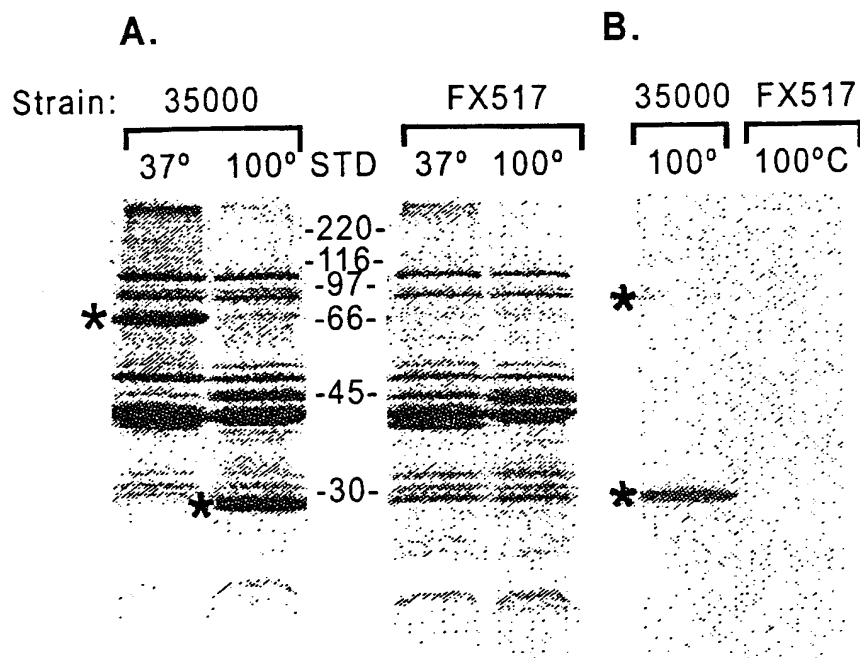


Fig. 6

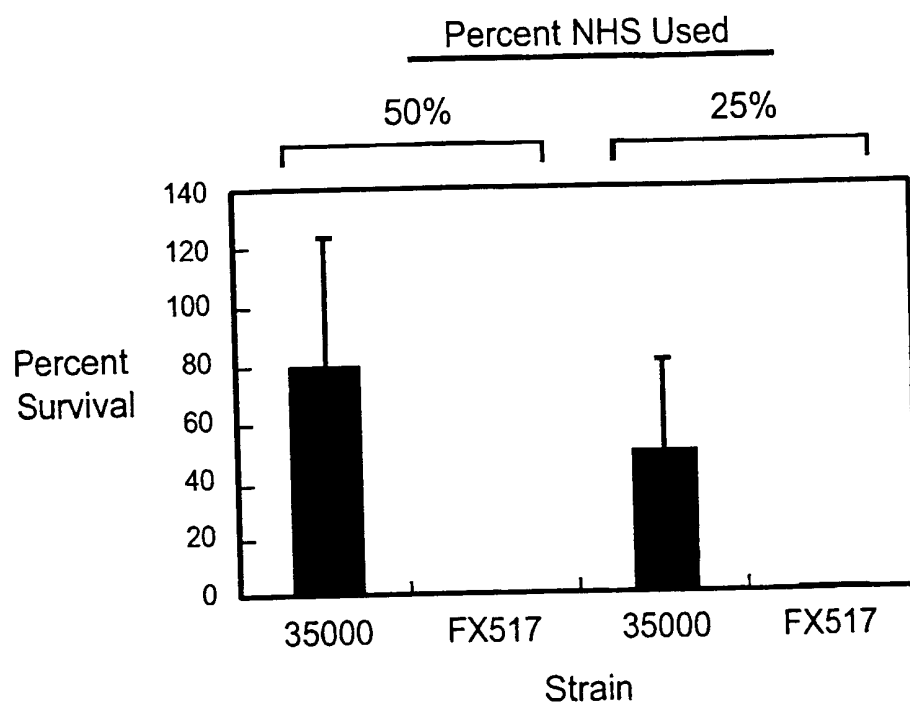


Fig. 7

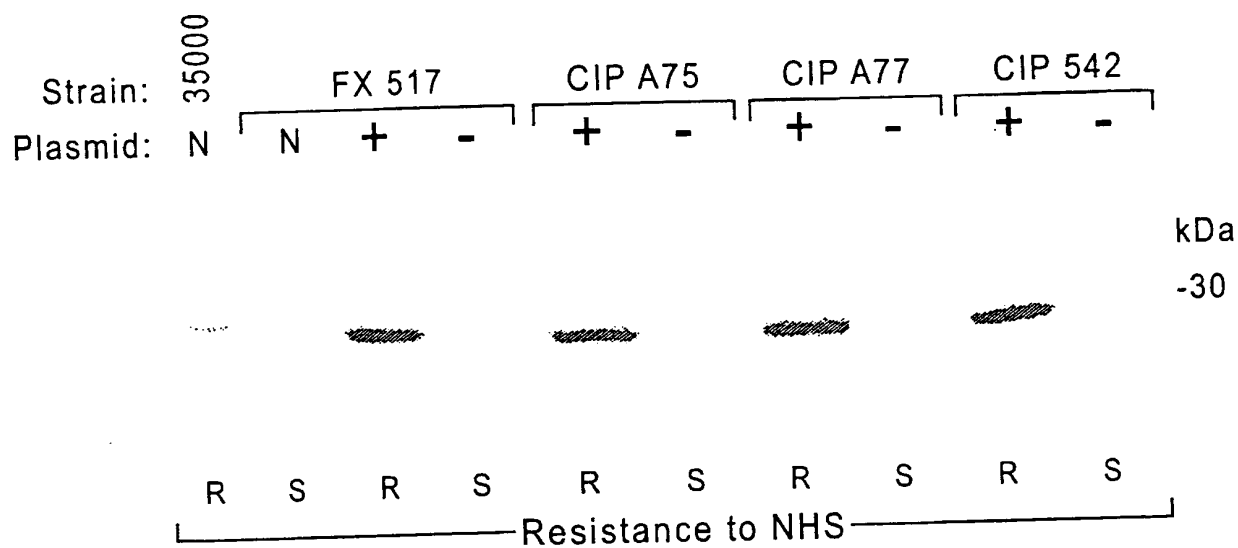
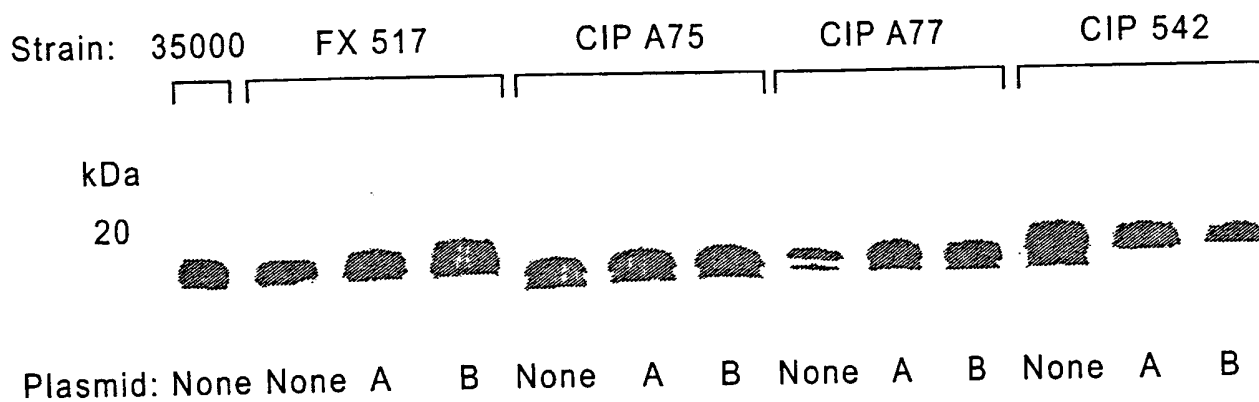


Fig. 8



9
b.
i.

* = Variable Region 1

= Variable Region 2 (Repeat Region)

Fig. 10

	<u>-35</u>	<u>-10</u>	
35000	TTGACATTTTTTTTAATGTAAGGTAGAAT		
CIP A75	TTGACATTTTTTTTA-----AGGTAGAAT		
CIP A77	TTGACATTTTTTTTA-----AGGTAGAAT		
CIP 542 (CAN)	TTGACATTTTTTTTAATGTAAGGTAGAAT		
CIP 542 (CDC)	TTGACATTTTTTTTAATGTAAGGTAGAAT		
CHIA	TTGACATTTCTTTTAATGTAAGGTAAAAT		
V-1157	TTGACATTTTTTTTAATGTAAGGTAGAAT		
M90-02	TTGACATTTTTTTTAATGTAAGGTAGAAT		
406	TTGACATTTTTTTTAATGTAAGGTAGAAT		
	10	20	30

Fig. 11

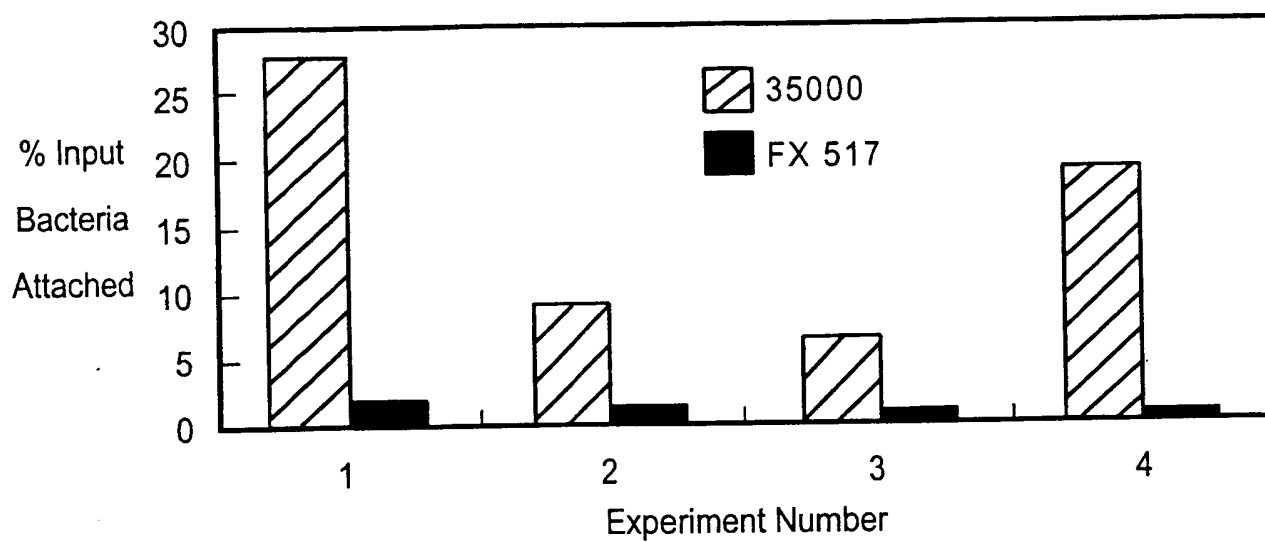
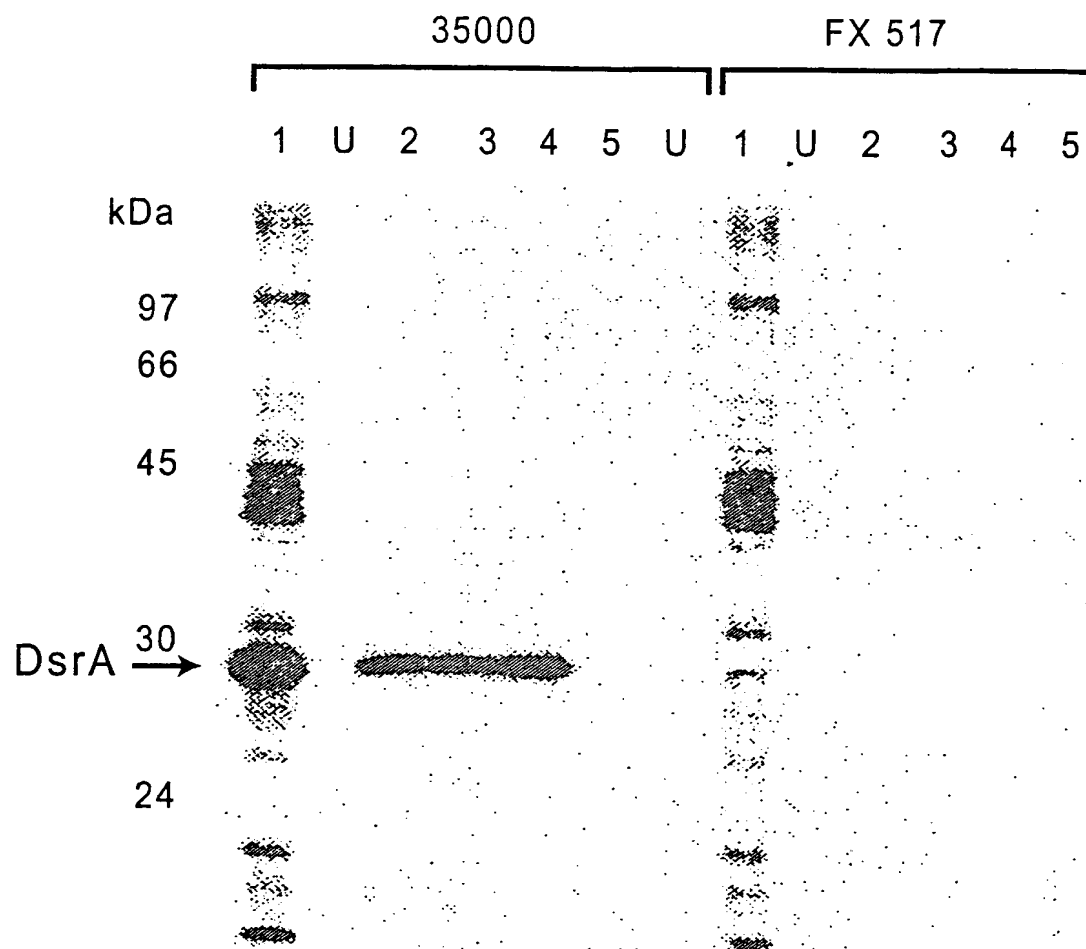


Fig. 12



U = Unlabeled OMP

1 = Surface-labeled *H. ducreyi* total protein

2 = Affinity purification, human native Vn

3 = Affinity purification, human recombinant Vn

4 = Affinity purification, bovine native Vn